28. A method according to claim 27, characterized in that each probe is distinguished from the other(s).

29. A method according to claim 27, characterized in that each probe is distinguished from the other(s) by having distinguishing mobility characteristics through a separating gel.

30. A method according to claim 27, characterized in that the plurality of different probes comprises a predetermined set of different probes each chosen to be specific for a respective target nucleic acid sequence.

31. A method according to claim 30, characterized in that the set comprises probes suitable to screen a plurality of different nucleic acid sequences simultaneously or substantially simultaneously such that determination of the quantity of each probe product produced enables quantitative determination of the copy number of the respective sequences in the sample.

32. A method according to claim 27, characterized in that the polymerase chain reaction is used to determine the quantity of each probe product produced.

33. A method according to claim 27, characterized in that the method is used to screen sequences of different genes or different sequences within a gene.

34. A method according to claim 27, characterized in that the method is used to screen sequences of different exons in a eukaryotic gene.

35. A method according to claim 27, characterized in that the method is used to detect genetic alterations.

36. A method according to claim 27, characterized in that the method is used to detect genetic deletions (reductions in sequence copy number) or genetic amplification (increases in sequence copy number).

37. A method according to claim 27, characterized in that the genetic material is immobilized prior to hybridization, such that hybridization flanking primers are likewise immobilized.

38. A method according to claim 27, characterized in that an excess of probes is used.

39. A method according to claim 27, characterized in that probes labelled for ready identification are used.

40. A method according to claim 27, characterized in that probes labelled with fluorescent labels are used.

41. A method according to claim 30, characterized in that more than one set of probes is used, either simultaneously or sequentially.

42. A method according to claim 30, characterized in that more than one set of probes is used and flanking primer pairs are the same for each set of probes.

43. A method according to claim 30, characterized in that more than one set of probes is used and flanking primer pairs are different for each set of probes.

44. A method according to claim 27, characterized in that the method comprises means to obviate or mitigate hybridization between primer binding sequences.

45. A method according to claim 27, characterized in that competing oligonucleotides are introduced to the sample.

46. A method according to claim 27, characterized in that competing oligonucleotides are introduced to the sample during the hybridization stage to releasably bind to primer binding sites flanking each probe to mitigate primer binding site interactions.

47. A method according to claim 27, characterized in that unbound probes and primers are thoroughly washed away from bound probes following hybridization and prior to analysis.

48. A method according to claim 27, characterized in that the method is used to screen one or more of DNA, RNA and cDNA with appropriate probe sets.

49. A method according to claim 27, characterized in that the method is used to screen one or more of somatic and germline sequences.

50. A method according to claim 27, characterized in that the method is used to screen for polymorphic alterations.

51. A set of probes adapted for use in performing the method according to claim 27.

52. A kit for performing the method according to claim 27 comprising a probe set, amplification primers and means to enable amplification and analysis of amplification product(s).